

**IN THE CLAIMS:**

Claims 1-13: (canceled)

Claim 14. (newly amended) A method for generating a high-dimensional vector ~~for at least one of a plurality of biopolymer materials represented in a set of sequence data, the method comprising:~~

~~for at least one of a plurality of biopolymer materials represented in a set of sequence data, which sequence data lacks ascertainable attributes, comparing sequence data regarding each biopolymer material to sequence data regarding each other biopolymer material to provide a respective comparison result;~~

arranging the comparison results in a square matrix indexed by the plurality of biopolymer materials;

creating a high-dimensional context vector for ~~at least~~ one of the biopolymer materials based on a row or column of the square matrix; and

~~creating a comparison matrix based on wherein the context vector provides attributes to enable visualization of the sequence data of the respective biopolymer material.~~

Claim 15. (previously amended) The method according to claim 14, wherein from each row or column of the square matrix, a respective high-dimensional context vector is created for each of the biopolymer materials based on the comparison results in the row or column.

FINNEGAN  
HENDERSON  
FARABOW  
GARRETT &  
DUNNER LLP

1300 I Street, NW  
Washington, DC 20005  
202.408.4000  
Fax 202.408.4400  
www.finnegan.com

Claim 16. (previously amended) The method according to claim 14, wherein the comparing uses a Basic Local Alignment Search Tool.

Claim 17. (previously amended) The method according to claim 14, wherein the comparing provides comparison results based on an expectation of a relation.

Claim 18. (currently reinstated, as previously amended) The method according to claim 14, wherein the biopolymer material is protein.

Claim 19. (previously amended) The method according to claim 14, wherein the biopolymer material is nucleic acid.

Claim 20. (currently amended) An apparatus for generating a high-dimensional vector ~~for at least one of a plurality of biopolymer materials represented in a set of sequence data, the apparatus comprising:~~  
~~at least one memory having program instructions, and~~  
~~at least one processor configured to execute the program instructions to perform the operations of:~~

for at least one of a plurality of biopolymer materials represented in a set of sequence data, which sequence data lacks ascertainable attributes, comparing sequence data regarding each biopolymer material to sequence data regarding each other biopolymer material to provide a respective comparison result;

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arranging the comparison results in a square matrix indexed by the plurality of biopolymer materials;

creating a high-dimensional context vector for at least one of the biopolymer materials based on a row or column of the square matrix; and

~~creating a comparison matrix based on wherein the context vector provides attributes to enable visualization of the sequence data of the respective biopolymer material.~~

Claim 21. (currently amended) An apparatus for generating a high-dimensional vector for ~~at least one of a plurality of biopolymer materials represented in a set of sequence data, the apparatus comprising:~~

for at least one of a plurality of biopolymer materials represented in a set of sequence data, which sequence data lacks ascertainable attributes, means for comparing sequence data regarding each biopolymer material to sequence data regarding each other biopolymer material to provide a respective comparison result;

means for arranging the comparison results in a square matrix indexed by the plurality of biopolymer material;

means for creating a high-dimensional context vector for at least one of the biopolymer materials based on a row or column of the square matrix; and

~~means for creating a comparison matrix based on wherein the context vector provides attributes to enable visualization of the sequence data of the respective biopolymer material.~~

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Claim 22. (currently amended) A computer-readable medium containing instructions for controlling a computer system to perform a method for generating a high-dimensional vector ~~for at least one of a plurality of biopolymer materials represented in a set of sequence data, the method comprising:~~

~~for at least one of a plurality of biopolymer materials represented in a set of sequence data, which sequence data lacks ascertainable attributes, comparing sequence data regarding each biopolymer material to sequence data regarding each other biopolymer material to provide a respective comparison result;~~

arranging the comparison results in a square matrix indexed by the plurality of biopolymer materials;

creating a high-dimensional context vector for at least one of the biopolymer materials based on a row or column of the square matrix; and

~~creating a comparison matrix based on wherein the context vector provides attributes to enable visualization of the sequence data of the respective biopolymer material.~~

Claim 23. (new) The method of claim 14, wherein the context vector is utilized for comparison of the biopolymer materials using cluster analysis.

Claim 24. (new) The method of claim 14, wherein the context vector comprises a row or column of an object attribute matrix of comparison results.

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GARRETT &  
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